Claim 11 was amended to recite a "G" at nucleotide 8933, rather than a "C." After a review of the sequence information given in the specification, applicants discovered this inadvertent error. See Figures 12 and 26. Because the foregoing amendment does not introduce new matter, entry thereof by the Examiner is respectfully requested.

Claims 11 and 12 were rejected under 35 U.S.C. § 101 because the invention as claimed allegedly lacks patentable utility and as disclosed is allegedly inoperative for reasons given in Paper No. 7. Office Action at 2. Applicants respectfully traverse this ground for rejection.

The present invention is directed to a nucleic acid of HIV-1 corresponding to the LTR region of the virus. This nucleic acid can be used, for example, as a probe in hybridization assays to detect the presence of nucleic acid of HIV-1 in a biological sample. Specification at page 14, lines 17-32. The presence of such nucleic acid is, of course, indicative of infection of HIV-1.

To sustain a rejection for lack of utility, it must be shown that the claimed invention is "totally incapable of achieving a useful result . . ." Brooktree Corp. v. Advanced Micro Devices, Inc., 24 U.S.P.Q.2d 1401, 1412 (Fed. Cir. 1992) (citations omitted). The Examiner has not met this burden.

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In maintaining the rejection for alleged lack of utility, the Examiner stated that applicants have not demonstrated that the LTR region is useful as a probe to detect HIV because

> HIV has not been specifically detected by using the nucleic acid sequence as claimed. Applicant is provided with a reference by Hahn et al. [Nature 312:166-169 (1984)] which demonstrates that at the time of the filing of the instant application, it was known that cross-hybridization occurs between the sequences of the LTR of HIV and those of other human retroviruses under certain hybridization conditions.

Office Action at 3-4. Applicants courteously disagree.

Applicants claim a nucleic acid corresponding to the complete LTR of HIV-1. Hahn et al. do not teach cross-hybridization between nucleic acids corresponding to the complete LTR of HIV-1, HTLV-I, and HTLV-II.

Hahn et al. refer to a hybridization experiment in which nucleic acid fragments of two strains of HTLV-I, HTLV-I and HTLV-Ib, and one strain of HTLV-II, were first separated on Southern blots. The fragments were then hybridized with the full-length HTLV-III clone. Hahn et al. at 168.

Hahn's results showed that a restriction fragment of HTLV-Ib containing exclusively pX sequences, and a corresponding fragment of HTLV-I containing pX and LTR sequences, faintly

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hybridized with the full-length HTLV-III clone. Hahn et al. at 168. HTLV-I and -II fragments containing LTR or envelope sequences did not hybridize to the HTLV-III probe:

> pX sequences of HTLV-II did not hybridize to the HTLV-III probe in the same stringency conditions, nor did fragments containing the LTR or envelope sequences of both HTLV-I and HTLV-II.

Hahn et al. at 168.

This experimental data indicates that the hybridization of the restriction fragment of HTLV-I containing pX and LTR sequences was due to the presence of the pX sequences and not to the presence of the LTR sequences.

This conclusion is supported by the findings of Arya et al. reported in "Homology of Genome of AIDS-Associated Virus With Genomes Of Human T-Cell Leukemia Viruses," Science, 225, 927-930 (1984) (Exhibit 1). This reference, which was published before the filing date of this application notes that while the present study did not allow the researchers to compare specifically the LTR of HTLV-III to those of HTLV-I and -II, the "weak signal obtained with 5' and 3' ultimate fragments containing the LTR suggest that these elements have minimal or no homology." Ayra et al. at 929.

Additional support for the uniqueness of the LTR region of HIV-1 is given in Starcich et al., "Characterization of Long Terminal Repeat Sequences of HTLV-III," Science, 227, 538-540 (1985) (Exhibit 2). The LTR of HTLV-III is 634 nucleotides in length, while the LTRs of HTLV-I and -II are 754 and 763 nucleotides in length, respectively. See Table 1, page 539 of

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Starcich et al. Thus, the LTR of HTLV-III can differ in length by 19% from the LTR of HTLV-I, and by 20% from the LTR of HTLV-II. The lengths of the U3, R, and U5 regions of the LTR also vary between HTLV-III and HTLV-I and -II. See Table 1, page 539 of Starcich et al.

Accordingly, the claimed nucleic acid corresponding to the LTR region of HIV-1, when used as a probe in a hybridization assay, would be expected to specifically detect the presence of HIV-1.

Continuing, the Examiner stated that the present invention lacks utility because although the specification teaches that the claimed nucleic acid is useful as a probe to detect the presence of HIV-1 in a biological sample (page 14, lines 17-32), hybridization conditions "which demonstrate a useful probe to detect HIV specifically are not set forth." Office Action at 3. Applicants disagree.

The specification need not include that which is already known by and available to the public. Paperless Accounting, Inc. v. Bay Area Rapid Transit System, 804 F.2d 659, 664 (Fed. Cir. 1986). In fact, techniques that were old and well-known when the application was filed need not be included in the specification, and are preferably omitted. Spectra-Physics, Inc. v. Coherent, Inc., 827 F.2d 1524, 1534 (Fed. Cir. 1987).

Because hybridization techniques were well known in the art at the time the application was filed, such techniques do not need to be described in the specification to establish utility for the claimed invention.

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For example, applicants teach in the specification that hybridization assays using nucleic acid probes have already been developed for Hepatitis B virus. Specification at page 14, lines 29-32. In addition, Hahn et al., published November 8, 1994, describe the use of an HTLV probe in hybridization assays. Hahn et al. at 168. Arya et al., published August 31, 1984, also describe hybridization experiments between HTLV-I and -II and HTLV-III.

Moreover, the use of a probe corresponding to the U3 and R regions of the LTR of HIV-1 in a hybridization assay to detect the presence of HIV-1 in a biological sample is discussed in Alizon et al., "Molecular Cloning of Lymphadenopathy-Associated Virus," Nature, 312, 757-760 (1984) (Exhibit 3). This reference was published on December 20/27, 1984, and was submitted for publication September 20, 1984.

pLAV13, a recombinant carrying an insert coding for the R and U3 regions of the LTR of LAV, a strain of HIV-1, was used as a probe in a series of filter hybridization experiments. Uninfected cultures and DNA from uninfected lymphocytes or from normal liver proved negative when screened with the probe under the same hybridization conditions. However, Southern blots of LAV-infected T-lymphocytes and CEM cells showed positive results when screened with the probe. Alizon et al. at 758.

Thus, as of September 20, 1984, one of skill in the art was capable of using an HIV-1 probe in hybridization assays to detect the presence of HIV-1 in a biological sample.

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Because the claimed invention is useful as a nucleic acid probe in hybridization assays to detect the presence of HIV-1, the withdrawal of this ground for rejection is respectfully requested.

It is acknowledged that this amendment is submitted after final rejection of the application. Because this amendment is belived to place the application in condition for allowance, applicants respectfully request entry thereof by the Examiner.

It is courteously submitted that this application is now in condition for allowance. Reconsideration and reexamination of this application, and allowance of the pending claims at the Examiner's convenience, are respectfully requested.

The Commissioner is hereby authorized to charge any fees associated with this Amendment to our Deposit Account No. 06-0916.

Respectfully submitted,

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